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Crystallographic structures of the elastase of *Pseudomonas aeruginosa*.

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The elastase protein of *Pseudomonas aeruginosa* is a zinc metalloprotease which has been shown to be a member of the bacterial neutral protease family. Its overall tertiary structure is similar to that of thermolysin. The x-ray crystallographic structure of the elastase has been solved to high resolution in three different crystal forms. Substantial conformational differences are observed in the protein in different crystal forms. In the absence of ligand, and independently in the presence of a covalent noncompetitive inhibitor, the elastase is observed to have a relatively "open" substrate binding cleft, while in the presence of tight-binding competitive inhibitors, the active site cleft is "closed".

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